IN THE CLAIMS

**Please amend claims 1 and 8-18, and add new claims 19 and 20 as shown below.**

1. (Currently amended) A method of detecting *Mycobacterium* species present in a biological sample, comprising the steps of:

providing a biological sample containing nucleic acid from at least one *Mycobacterium* species comprising a *Mycobacterium* 16S ribosomal RNA (rRNA) or DNA encoding *Mycobacterium*16S rRNA;

amplifying the *Mycobacterium* 16S rRNA or *Mycobacterium* DNA in an in vitro nucleic acid amplification mixture comprising at least one polymerase activity, and a combination of at least two primers having sequences selected from the group consisting of a first primer of SEQ ID NO:11 and a second primer that is an oligonucleotide consisting of 19 to 25 bases, containing 18 contiguous bases of SEQ ID NO:24 and three to seven bases 5' to the 18 contiguous bases of SEQ ID NO:24 ~~SEQ ID NO:1 to SEQ ID NO: 34, SEQ ID NO:37 and SEQ ID NO:38~~ to produce amplified *Mycobacterium* nucleic acid; and

detecting the amplified *Mycobacterium* nucleic acid by detecting a label associated with the amplified *Mycobacterium* nucleic acid.

2. (Original) The method of Claim 1, further comprising in the steps of:

adding to the biological sample at least one capture oligonucleotide that specifically hybridizes to the *Mycobacterium* 16S rRNA and an immobilized nucleic acid that hybridizes to the capture oligonucleotide under hybridizing conditions to produce a hybridization complex; and

separating the hybridization complex from other components of the biological sample before the amplifying step.

3. (Original) The method of Claim 1, wherein the amplifying step amplifies 16S rRNA or DNA encoding 16S rRNA from *M. tuberculosis* or a *Mycobacterium* other than *tuberculosis* (MOTT) species.

4. (Original) The method of Claim 1, wherein the amplifying step amplifies 16S rRNA or DNA encoding 16S rRNA from *M. abscessus, M. africanum, M. asiaticum, M. avium, M. bovis, M. celatum, M. chelonae, M. flavescens, M. fortuitum, M. gastri, M. gordonae, M. haemophilum, M. intracellulare, M. interjectum, M. intermedium, M. kansasii, M. malmoense, M. marinum, M. non-chromogenicum, M. paratuberculosis, M. phlei, M. scrofulaceum, M. shimodei, M. simiae, M. smegmatis, M. szulgai, M. terrae, M. triviale, M. tuberculosis, M. ulcerans* or *M. xenopi.*

5. (Original) The method of Claim 1, wherein the detecting step uses at least one probe that hybridizes specifically to the amplified *Mycobacterium* nucleic acid.

6. (Original) The method of Claim 5, wherein the detecting step uses at least one labeled probe that hybridizes specifically to the amplified *Mycobacterium* nucleic acid.

7. (Original) The method of Claim 5, wherein the detecting step uses a plurality of probes that hybridize specifically to the amplified *Mycobacterium* nucleic acid.

8. (Currently amended) The method of Claim 1, wherein the amplifying step uses a combination of at least a first primer and a second primer, wherein the first primer is SEQ ID NO:11 ~~selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12~~, and the second primer is selected from the group consisting of SEQ ID NO:21, SEQ NO:22, SEQ ID NO:23 and SEQ ID NO:24 ~~SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 and SEQ ID NO:38~~.

9. (Currently amended) The method of Claim 8, wherein the amplifying step uses a combination of ~~at least~~ a first primer and a second primer, wherein ~~the first primer is selected from the group consisting of SEQ ID NO:7 to SEQ ID NO:12, and~~ the second primer is SEQ ID NO:21. ~~selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 and SEQ ID NO:38.~~

10. (Currently amended) The method of Claim 8, wherein the amplifying step uses a combination of ~~at least~~ a first primer and a second primer, wherein the second primer is SEQ ID NO:22. ~~selected from the group consisting of:~~

~~the first primer having the sequence of SEQ ID NO:7, and the second primer having the sequence of SEQ ID NO:13;~~

~~the first primer having the sequence of SEQ ID NO:7, and the second primer having the sequence of SEQ ID NO:14;~~

~~the first primer having the sequence of SEQ ID NO:7, and the second primer having the sequence of SEQ ID NO:15;~~

~~the first primer having the sequence of SEQ ID NO:7, and the second primer having the sequence of SEQ ID NO:16;~~

~~the first primer having the sequence of SEQ ID NO:8, and the second primer having the sequence of SEQ ID NO:13;~~

~~the first primer having the sequence of SEQ ID NO:8, and the second primer having the sequence of SEQ ID NO:14;~~

~~the first primer having the sequence of SEQ ID NO:8, and the second primer having the sequence of SEQ ID NO:15;~~

~~the first primer having the sequence of SEQ ID NO:9, and the second primer having the sequence of SEQ ID NO:13;~~

~~the first primer having the sequence of SEQ ID NO:9, and the second primer having the~~

~~sequence of SEQ ID NO:14;~~

~~the first primer having the sequence of SEQ ID NO:9, and the second primer having the sequence of SEQ ID NO:15;~~

~~the first primer having the sequence of SEQ ID NO:10, and the second primer having the sequence of SEQ ID NO:16;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:13;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:16;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:17;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:18;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:19;~~

~~the first primer having the sequence of SEQ ID NO:11, and the second primer having the sequence of SEQ ID NO:20; and~~

~~the first primer having the sequence of SEQ ID NO:12, and the second primer having the sequence of SEQ ID NO:15.~~

11. (Currently amended) The method of Claim 8, wherein the amplifying step uses a combination of the first primer ~~having the sequence of SEQ ID NO:11,~~ and the second primer, wherein the second primer is SEQ ID NO:23. ~~having the sequence of SEQ ID NO:16, SEQ ID NO:30 or SEQ ID NO:37.~~

12. (Currently amended) The method of Claim 8, wherein the amplifying step uses a combination of the first primer and the second primer, wherein the second primer is SEQ ID NO:24. ~~having the sequence of SEQ ID NO:11, and two second primers having the sequences SEQ ID NO:16 and SEQ ID NO:37.~~

13. (Currently amended) A composition for amplifying in an in vitro amplification reaction a *Mycobacterium* 16S rRNA sequence or a DNA encoding 16S rRNA, comprising a combination of at least two oligonucleotides, wherein a first oligonucleotide contains a promoter sequence and a sequence that hybridizes to a *Mycobacterium* 16S rRNA or DNA sequence, and a second oligonucleotide is an oligonucleotide consisting of 19 to 25 bases, containing 18 contiguous bases of SEQ ID NO:24 and three to seven bases 5' to the 18 contiguous bases of SEQ ID NO:24. ~~one or more oligonucleotides having a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO: 34, SEQ ID NO:37 and SEQ ID NO:38~~.

14. (Currently amended) The composition of Claim 13, wherein the composition comprises:

at least one first oligonucleotide having the sequence of SEQ ID NO:11 ~~any one of SEQ ID NO:1 to SEQ ID NO:12~~, and

at least one second oligonucleotide having the sequence of any one of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 and SEQ ID NO:24. ~~SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 or SEQ ID NO:38.~~

15. (Currently amended) The composition of Claim 14, wherein the composition comprises:

at least one first oligonucleotide ~~containing the sequence of any one~~ of SEQ ID NO:11 ~~7 to SEQ ID NO:12~~, and

at least one second oligonucleotide of SEQ ID NO:21. ~~containing the sequence of any one of SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 or SEQ ID NO:38~~.

16. (Currently amended) A kit containing one or more oligonucleotides having a sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24. ~~SEQ ID NO:1 to SEQ ID NO:34, SEQ ID NO:37 and SEQ ID NO:38~~.

17. (Currently amended) The kit of claim 16, further containing an oligonucleotide of SEQ ID NO:11.

~~at least one first oligonucleotide having the sequence of any one of SEQ ID NO:1 to SEQ ID NO:12, and~~

~~at least one second oligonucleotide having the sequence of any one of SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 or SEQ ID NO:38.~~

18. (Currently amended) The kit of claim 17, containing

at least one first oligonucleotide of SEQ ID NO:11 ~~containing the sequence of any one of SEQ ID NO:7 to SEQ ID NO:12~~, and

at least one second oligonucleotide ~~containing the sequence~~ of any one of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 or SEQ ID NO:25. ~~SEQ ID NO:13 to SEQ ID NO:34, SEQ ID NO:37 or SEQ ID NO:38.~~

19. (New) The composition of Claim 14, wherein the composition comprises:

at least one first oligonucleotide of SEQ ID NO:11, and

at least one second oligonucleotide of SEQ ID NO:23.

20. (New) The composition of Claim 14, wherein the composition comprises:

at least one first oligonucleotide of SEQ ID NO:11, and

at least one second oligonucleotide of SEQ ID NO:24.

**Comments**

This application is a divisional of U.S. Application No. 09/738,274, filed December 15, 2000, and claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Application No. 60/172,190, filed December 17, 1999, the contents of both of which have been incorporated by reference in the present application. The substitute specification filed with this application is identical to the parent application except that the "Related Applications" section that appears at page 1, lines 2-5, has been amended to insert the information described in the previous sentence.

Applicants have not filed a computer readable Sequence Listing with this divisional application because the Sequence Listing is identical to the Sequence Listing filed with the '274 application. Applicants request that the computer readable Sequence Listing provided with the '274 application be used in this application. If a substitute computer readable form of the Sequence Listing is required, Applicants request that the request for it be made of Applicants' representative at the telephone number provided below.

The parent application (No. 09/738,274) was subject to a restriction and species requirements (Paper No.3, mailed 02/27/2002). In response, Applicants elected composition claims and the species (i.e., a single primer pair) of SEQ ID NO:5 and SEQ ID NO:34.

In this divisional application, Applicants present claims for examination based on the species of SEQ ID NO:24, which is used in combination with another primer which is a promoter primer (e.g., SEQ ID NO:11), as described, for example in Example 3 (pages 17-19) of the specification. SEQ ID NO:24 is structurally related to other sequences disclosed in the specification (SEQ ID Nos 1-23) as shown below.

| SEQ ID | | LENGTH |
|---|---|---|
| 21 | gcaagtcgaacggaaaggcctttcg | 25 |
| 22 | caagtcgaacggaaaggcctttcg | 24 |
| 23 | gtcgaacggaaaggcctttcgg | 22 |
| 24 | gaacggaaaggcctttcgg | 19 |

Based on this structural relationship, the claims have been amended generally to recite "an oligonucleotide consisting of 19 to 25 bases, containing 18 contiguous bases of SEQ ID NO:24 and three to seven bases 5' to the 18 contiguous bases of SEQ ID NO:24" which describes this structural relationship. Dependent claims specifically recite the SEQ ID Nos of embodiments of these oligonucleotides.

In this preliminary amendment, claims 1 and 8-18 have been amended and claims 19 and 20 are new. The remaining claims (claims 2-7) are the original claims.

Applicants disclose to the Examiner a co-pending U.S. application (serial no. 09/738,972) for "Methods and Compositions for Detection of *Mycobacterium avium* Complex Species" which names as an inventor (S. Brentano) one of the co-inventors of this application.

These amendments are presented to place the application in better condition for examination. If minor matters related to initiating examination can be addressed by the Applicants' representative before a formal office action is mailed, the Examiner is requested to call Applicants' representative at the telephone number provided below.

I hereby certify that this correspondence is being deposited with the U.S. Postal Service on the date shown below with sufficient postage as Express Mail No. EV198142105US in an envelope addressed to Mail Stop Patent Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Respectfully Submitted,

Dated: September 18, 2003

By: Christine A. Gritzmacher

Christine A. Gritzmacher
Registration No. 40,627

GEN-PROBE INCORPORATED
Patent Department
10210 Genetic Center Drive
San Diego, CA 92121

Tel.: (858) 410-8926
FAX: (858) 410-8928

T:\legal\genprobe\GP107\03-DV\PrelimAmd091803